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DM of: US-09-438-185-1047 to: EST:*
date: Jun 29, 2001 2:24 PM
about: Results were produced by the GenCore software, version 4.5.
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Command line parameters:
-MODEL-frame+p2n.model -DEV=x1p
-Q-/c0r2_1/USPTO_spool/US09438185/runat_29062001_074544_6949/app_q
-DB=EST -QFRT=fastart -SUFFIX=rst -GAPOP=12_000 -GAPEXT=4_000
-MINMATCH=0_100 -LOOPCPL=0_000 -LQOPEXT=0_000 -QGAPOP=4_500
-QGAPENT=0_050 -XGAPOP=10_000 -AGAPEXT=0_500 -FGAPOP=6_000
-FGAPEXT=7_000 -YGAPOP=10_000 -YGAPEXT=0_500 -DELOP=6_000
-DELEXT=7_000 -START=1 -MATRIX_BLOSUM2 -THR_MAX=-100 -THR_MIN=0
-LIST=45 -DOCALIGN=200 -THR_SCORE_PCT -THR_MAX=-100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -PFS -NORM=ext -MINLEN=0
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-ICPU=3 -LONGLOG -NO_ALPPXY -WAIT -THREADS=1

Search information block:
Or US-09-438-185-1047
length: 362
Database: ESM:*
Database sequences: 10228115
Database length: 431459454
Search time (sec): 1175.810000

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mand line parameters:

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seq_documentation_block:
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  DEFINITION Stratagene Chick Embryo Lambda cDNA Library (* 937405)
  ACCESSION AL584678
  VERSION AL584678.1 GI:13163409
  SOURCE EST
  KEYWORDS chicken.
  ORGANISM Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianine; Gallus

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Search information block:
US-09-438-185-1047
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Database sequences: 10228115
Database length: 431459454
Search time (sec): 115.75 81/00000

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 242 CAGAGTGTACTACTAGTGTACCTACGGCTGGATCCTCTGT 291
 192 heSerLeuThrProAspLeuLeuHisAspLeuLeuGlyHisValProTrp 208
 292 ACACCCAGAACCGGATACATGCCATGAACTTGGACATGGCTCMA 341
 209 LeuLeuHisProSerPheSerGluPheLeuAsnMetGlyArgLeuPh 225
 342 CTTGGCTGATCCCTAACGTTGCCCAAGTTCAAGAGATAGGA 383
 225 erHrLysValLeuGluLysValGlnAlaLeuProSerLysGlnDArgI 242
 184 .CNCGCTTCACTGGAGCATCGACGAGATGAGATG 414
 412 leGlnTrhLeuGlnSerAsnLeuLeuAlaLeuLeuArgCysPheProPhe 258
 415 TICAGAAATTACCCACT. 443
 259 ThrValGluSerGlyLeuIleLeuAsnHisGluGlyArgLysSerArgI 275
 444 ACCTATGAACTGGCTCTGCTCTCTGCTACGGCTAACGCTACCGCTGCTATGG 493
 275 yAlaValLeuIleSerSerProGlnGluLenglyHisAlaPheLeuAspA 292
 494 GCGAGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTGACA 543
 292 svalValArgValLeuProLeuGluLeuAspGlnIleLeuArgLeuProPh 308
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 309 AsnThrSerThrProGlnLhrLysSerLeuSerIleArgLysPheAspG1 325
 594 CTTATCACCTTCAAGGCTTACTTGTCAAAAGTTNTGAGA 643
 325 uLeuValGlu 328
 644 AGCCAAAGAA 653

seq.name: gb.est14:AA968411
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 ORGANISM Mus house mouse.
 LOCATION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus
 REFERENCE 1 (bases 1 to 669)
 AUTHORS Marra, M., Hillier, L., Allen, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Scheibenbogen, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Watters, R.
 TITLE The WashU-HMMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra, M./Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES source This clone is available at CHGC in Shanghai.
 location/qualifiers 1. 107
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 /db_xref="taxon:9606"
 /clone="GLCBF06"
 /clone.lib="GLC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk (-); Site_1: ECORI; Site_2: XbaI"
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 Percent Identity: 28.502
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 US-09-438-185-1047 x AV650135
 Align seg 1/1 to: AV650135 from: 1 to: 607
 104 Arg Asn Leu Ile Tyr Arg Leu Leu Ser Arg Phe Ser Leu Tyr Lys 120
 34 AGAAAACATGGGGCACAGTGTCAGTCAGTCCTGAAAGCTCTATAAAC 83

seq_name: gb_est:0:AV650135

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 VERSION AV650135.1 GI:9871149
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS Qian,B., Wu,T., Huang,Q., Peng,Y., Liu,P., Qu,J., Song,H., Cheng,Z., Xu,Z., Xu,X., Li,N., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z., and Han,Z.
 TITLE Unpublished (2000)
 JOURNAL Contact: Zequang Han
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 Tel: 86-21-50801910(ex.45)
 Fax: 86-21-50801922
 Email: hanze@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 location/qualifiers 1. 107
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCBF06"
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 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
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 Percent Identity: 28.502
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 US-09-438-185-1047 x AV650135
 Align seg 1/1 to: AV650135 from: 1 to: 607
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 34 AGAAAACATGGGGCACAGTGTCAGTCAGTCCTGAAAGCTCTATAAAC 83

seq_name: gb_est:0:AV650135

seq_documentation_block:
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 DEFINITION C93803 Dictyostelium discoideum SS (M. Yoshida) Dictyostelium
 discoideum cDNA clone SSL848, mRNA sequence.
 ACCESSION C93803
 VERSION C93803.1 GI:3192312
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum.
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium
 1 (bases 1 to 729)
 REFERENCE Yoshida, M.
 AUTHORS Developmental cDNA in Dictyostelium discoideum (M. Yoshida)
 TITLE Unpublished (1998)
 JOURNAL Contact: Motonobu Yoshida
 COMMENT Research Institute of Food Science
 Kinki University
 Nakamachi 3327, Nara 631, Japan
 Email: Yoshida@ers06.nara.kindai.ac.jp
 Dictyostelium discoideum cDNA project in Japan.
 FEATURES 1. 729
 source Location/Qualifiers
 /organism="Dictyostelium discoideum"
 /organism="Dictyostelium discoideum"

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115-09-438-185-1047.rst

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 Quality: 184.50 Gaps: 6
 Ratio: 1.577 Percent Identity: 29.293
 Percent Similarity: 59.091

Percent Similarity: 59.091

alignment_block:
 US-09-438-105-1047 x AA880857

Align seg 1/1 to: AA880857 from: 1 to: 592

108 TyrArgLeuLeuSerSerArgPheSerLeuTrpLysserTyrCysProAr 124
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 5 TTTCAGGTCTTGACACCTGTATAAACACAGCCGCTAGAGACAR 54

124 gPhePheLeuAspPheTrpLeuGluLalaPhe...GLYLeuLeuSerAspHeL 140
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 55 CCACACATCCTCCTCTGAACTGAAAGTACTGCGGTTTCGTTGAAAGACACAA 104

140 euAsPhe...GlnAlaValLeuLeuPhePheGluLeuGluThrHisPhe 155
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
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156 SerTyrProValSerGlyPheValAlaProHisGlnTyrLeuSerLe 172
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 155 CGCTCCGTCCTGTTCTGCTTACTGCTCTCGAGATTCTGGGG 204

172 uLeuGlnAspArgTyrPheProlLeuAlaSerValMetArgThrLeuAsP 189
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 205 CCTGGCATTCGGATCCAGTCTCCACTGACACAGTACATAGCTAGCATGGCTTA 254

189 yAsPAsnPheSerLeuThrProAsPheLeuHisAspLeuLeuGlyHis 205
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206 ValProIProLeuHisProSerPheSerCluPhePheIleAsnMetG 222
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 305 GTGCCCTGTGTTTCAGTATAGAAGCTTGCCAGTTCTAGGAATTTGG 354

222 YAlgleuPheThrLysValIleGluLysValGlnAlaLeuProSerLysL 239
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239 YSGlnArgIleGlnThrLeuGlnSerAsnLeuLeuAlaIleValArgCys 255
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 378 ATGAGTACATTGAACTGGCCACA.....ATGATG 406

356 PheIrrPheThrValGluSerGlyLeuLeuGluAsnHisGluGlyArgY 272
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 407 TACGTGTTTAACTGNGAGTTGCGCTTGCAAGAAAGGAGTCATAAAA 456

272 SALaTyrGlyAlaValLeuIleSerSerProGlnGluLeuGlyHisAla. 288
 ::|||:|||:|||:|||:|||:|||:
 457 GGCATATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGAGATACTG...ACTG 503

289 PheIleAspAsnValoLArgValLeuProLeuGluLeuAspGln 302
 ::|||:|||:|||:|||:|||:|||:
 504 TTATAGACAGCCAGNTCCCTGCCCNNTGGAGCTAGAGAAG 545